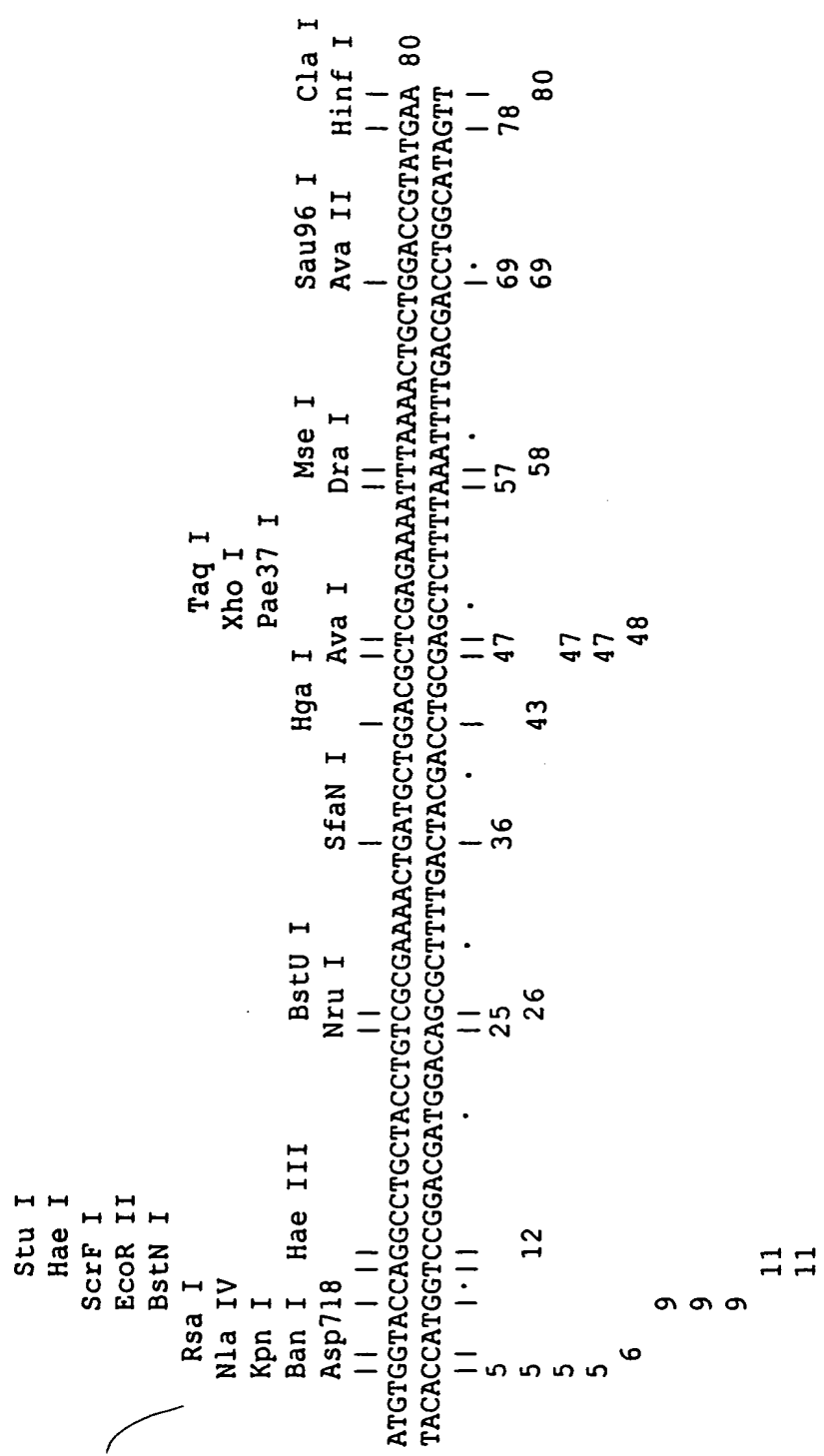


60222707051250

Fig. 1A

METOTP-1.SEQ4 -> Restriction Map

DNA sequence 540 b.p. ATGTGGTACCAG ... CCGTAAGGTACC linear





Scrf I  
PflM I  
Ecor II  
BstN I

Hae III

Hae I

Fee

Bal I

Spec I

Dec 1

1111

GCCTTGGGACACTACTCTTCTAGAACAACTGTGCACCTGGTCTGCAACAGCAACTGGACCATCTGGACACTTGGCGTGGCCA 320

CGAACCCTGTGATGAGAGATCTTGTGACACGTGACCAGACGTTGTCGTTGACCTGGTAGACCTGTGAACGGCACCGGT

.....

[illegible]

254	270	200	254
255	270	291	312

233	270	294	315
-----	-----	-----	-----

250	274	253
250	274	215

	E/7	CC7
CTC		
L3		

316

010 010 010

318

318  
319  
320

318  
319  
320

318

**Sau3A I**

# Mbo I

**Sau3A I**

**Mbo I**

**Dpn I**

# Alw I

# Nla IV

---

00227 0709460

**Fig. 1D**

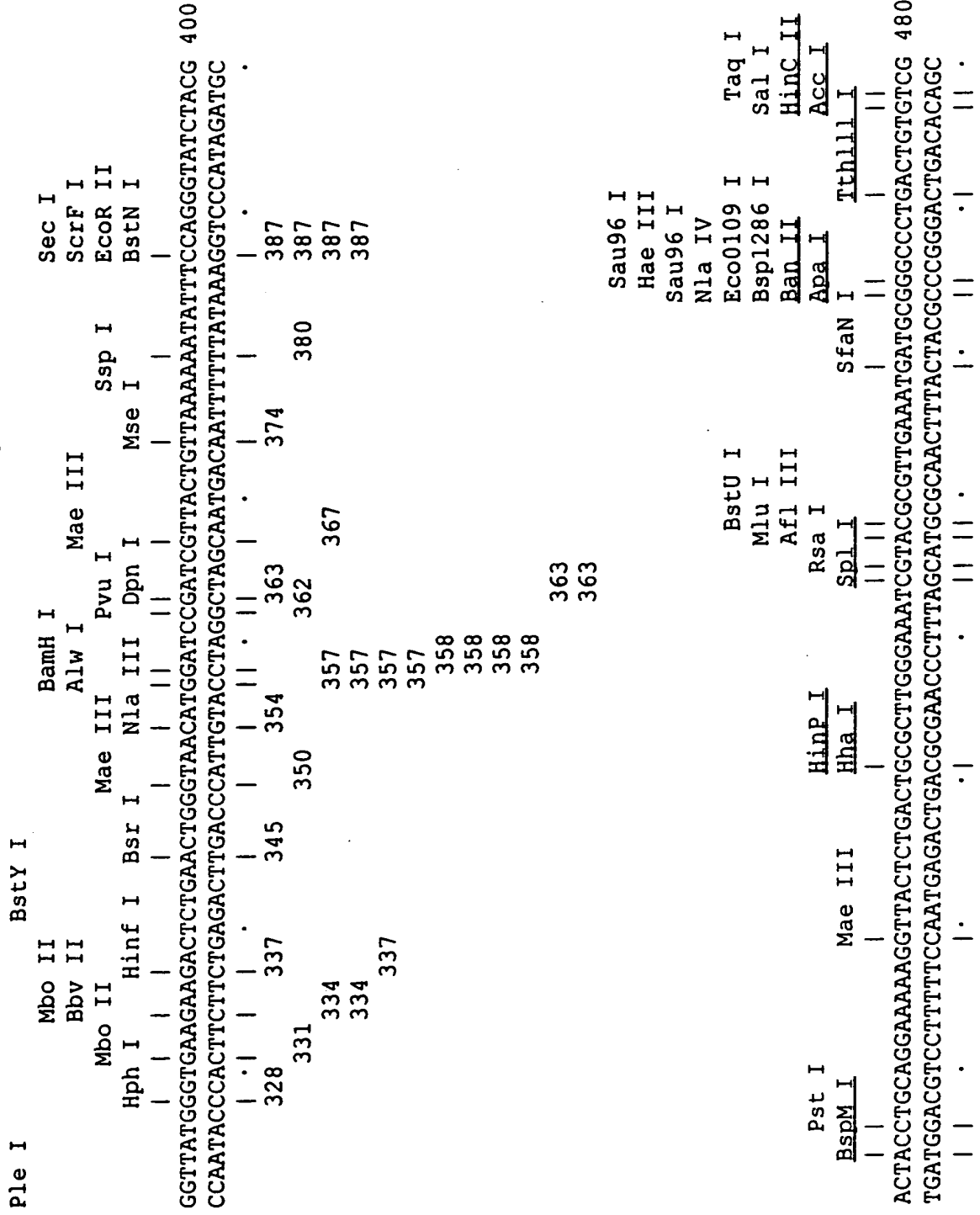
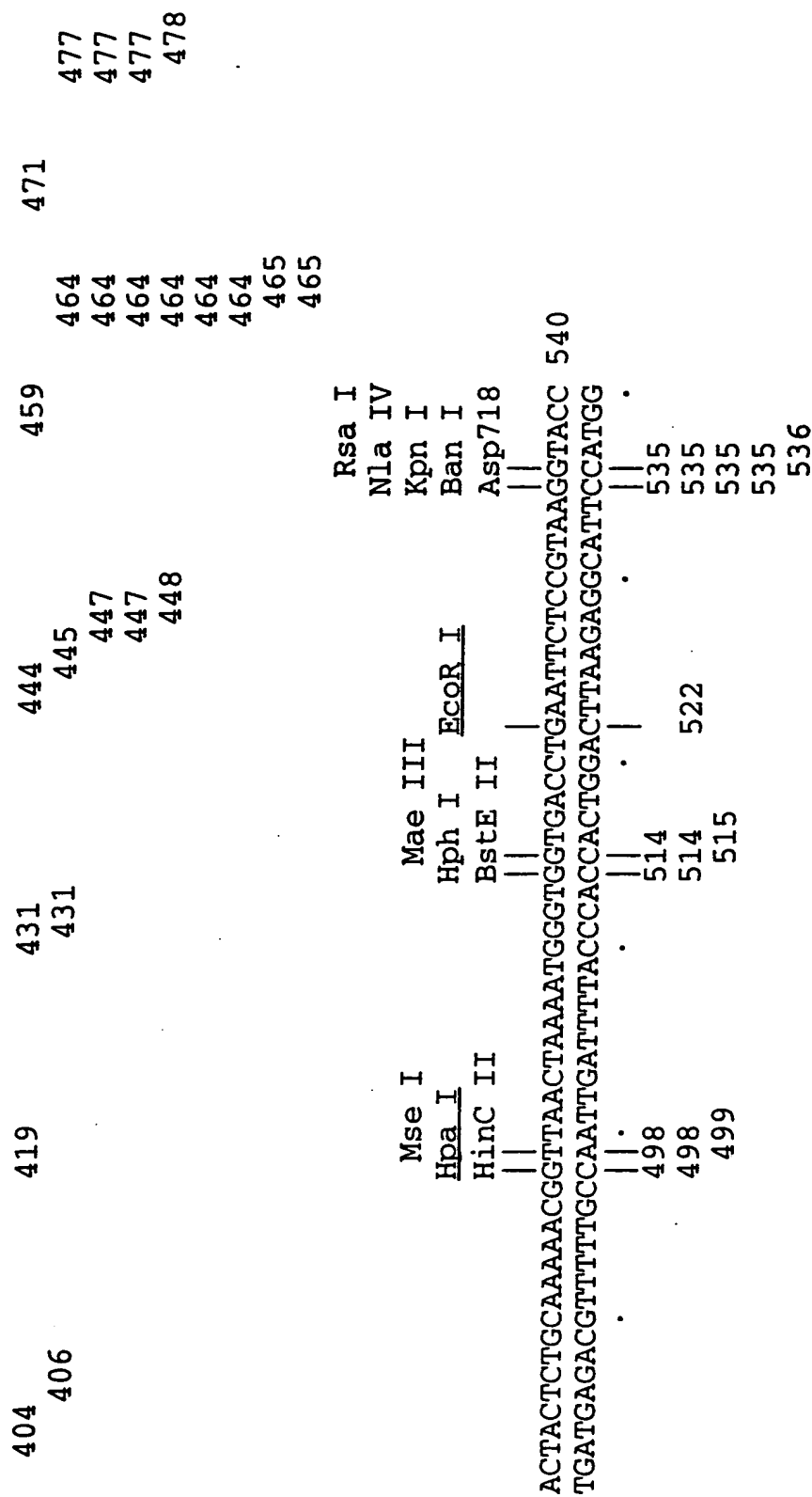


Fig. 1E



00222-61631463

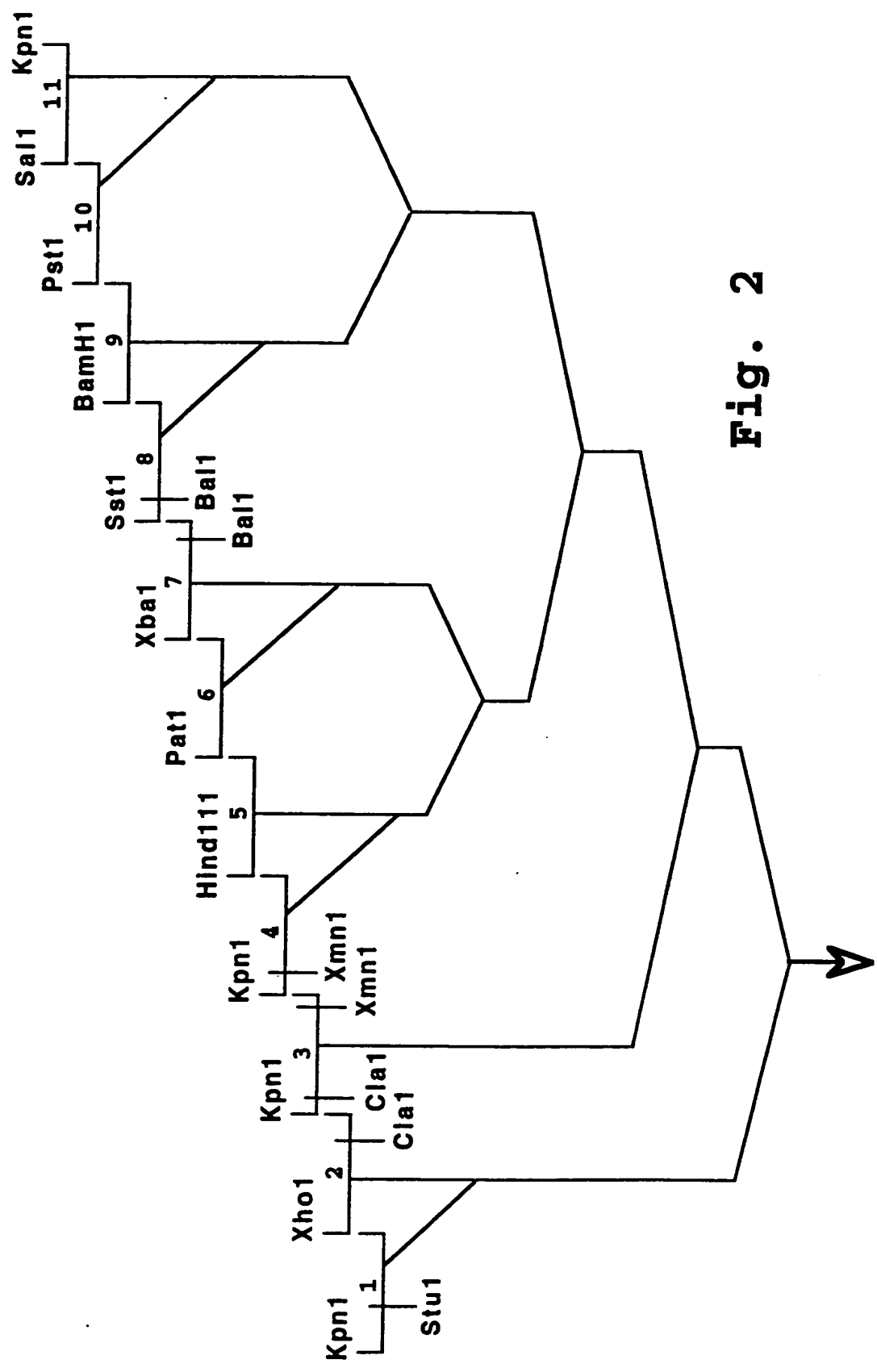
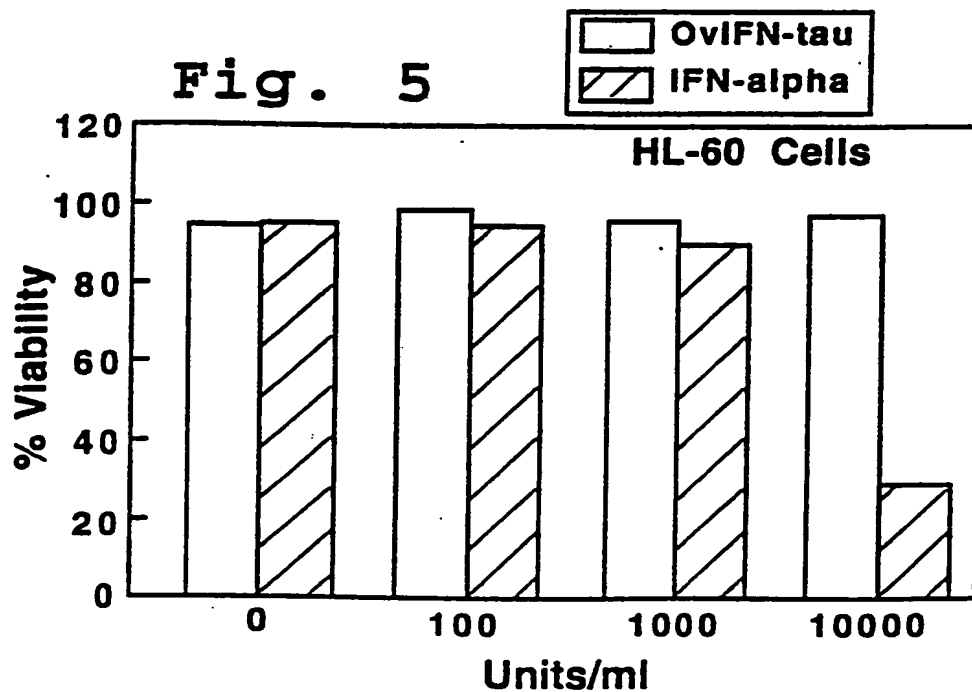
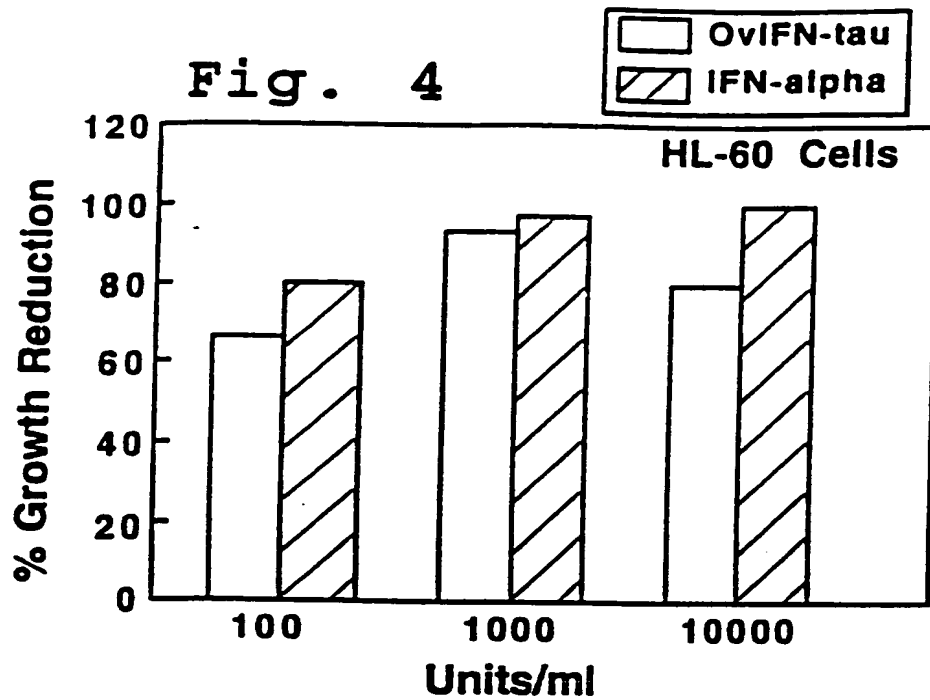


Fig. 2

-23 -9  
 met ala phe val leu ser leu leu met ala leu val leu val ser  
 oIFNt cccc ATG GCC TTC GTG CTC TCT CTA CTG ATG GCC CTG GTG CTG GTC AGC  
 htIFN cccc ATG GCC TTC GTG CTC TCT CTA CTC ATG GCC CTG GTG CTG GTC AGC  
  
 -8 -1 +1 11  
 tyr gly pro gly gly ser leu gly cys tyr leu ser arg lys leu met leu asp ala  
 TAT GGC CCA GGA GGA TCT CTG GGT TGT TAC CTA TCT CGG AAA CTC ATG CTG GAT GCC  
 TAC GGC CCA GGA GGA TCC CTG GGT TGT GAC CTG TCT CAG AAC CAC GTG CTG GTT GGC  
  
 12 20 30  
 arg glu asn leu lys leu leu asp arg met asn arg leu ser pro his ser cys leu  
 AGG GAG AAC CTC AAG CTC CTG GAC CGA ATG AAC AGA CTC TCC CCT CAT TCC TGT CTG  
 AGG AAG AAC CTC AGG CTC CTG GAC GAA ATG AGG AGA CTC TCC CCT CGC TTT TGT CTG  
  
 31 40 49  
 gln asp arg lys asp phe gly leu pro gln glu met val glu gly asp gln leu gln  
 CAG GAC AGA AAA GAC TTT GGT CTT CCC CAG GAG ATG GTG GAG GGC GAC CAG CTC CAG  
 CAG GAC AGA AAA GAC TTC GCT TTA CCC CAG GAA ATG GTG GAG GGC GGC CAG CTC CAG  
  
 50 60 68  
 lys asp gln ala phe pro val leu tyr glu met leu gln gln ser phe asn leu phe  
 AAG GAC CAG GCC TTC CCT GTG CTC TAC GAG ATG CTC CAG CAG AGC TTC AAC CTC TTC  
 GAG GCC CAG GCC ATC TCT GTG CTC CAT GAG ATG CTC CAG CAG AGC TTC AAC CTC TTC  
  
 69 70 80 87  
 tyr thr glu his ser ser ala ala try asp thr thr leu leu glu gln leu cys thr  
 TAC ACA GAG CAC TCC TCT GCT GCC TGG GAC ACC ACC CTC CTG GAG CAG CTC TGC ACT  
 CAC ACA GAG CAC TCC TCT GCT GCC TGG GAC ACC ACC CTC CTG GAG CAG CTC CGC ACT  
  
 88 90 100 106  
 gly leu gln gln gln leu asp his leu asp thr cys arg gly gln val met gly glu  
 GGA CTC CAA CAG CAG CTG GAC CAC CTG GAC ACC TGC AGG GGT CAA GTG ATG GGA GAG  
 GGA CTC CAT CAG CAG CTG GAC AAC CTG GAT GCC TGC CTG GGG CAG GTG ATG GGA GAG  
  
 107 110 120 125  
 glu asp ser glu leu gly asn met asp pro ile val thr val lys lys tyr phe gln  
 GAA GAC TCT GAA CTG GGT AAC ATG GAC CCC ATT GTG ACC GTG AAG AAG TAC TTC CAG  
 GAA GAC TCT GCC CTG GGA AGG ACG GGC CCC ACC CTG GCT CTG AAG AGG TAC TTC CAG  
  
 126 130 140 144  
 gly ile tyr asp tyr leu gln glu lys gly tyr ser asp cys ala trp glu ile val  
 GGC ATC TAT GAC TAC CTG CAA GAG AAG GGA TAC AGC GAC TGC GCC TGG GAA ATC GTC  
GGC ATC CAT GTC TAC CTG AAA GAG AAG GGA TAC AGC GAC TGC GCC TGG GAA ACC GTC  
  
 145 150 160 163  
 arg val glu met met arg ala leu thr val ser thr thr leu gln lys arg leu thr  
 AGA GTC GAG ATG ATG AGA GCC CTC ACT GTA TCA ACC ACC TTG CAA AAA AGG TTA ACA  
AGA CTG GAA ATC ATG AGA TCC TTC TCT TCA TTA ATC AGC TTG CAA GAA AGG TTA AGA  
  
 164 172  
 lys met gly gly asp leu asn ser pro end  
 AAG ATG GGT GGA GAT CTG AAC TCA CCT TGA  
ATG ATG GAT GGA GAC CTG AGC TCA CCT TGA

Fig. 3



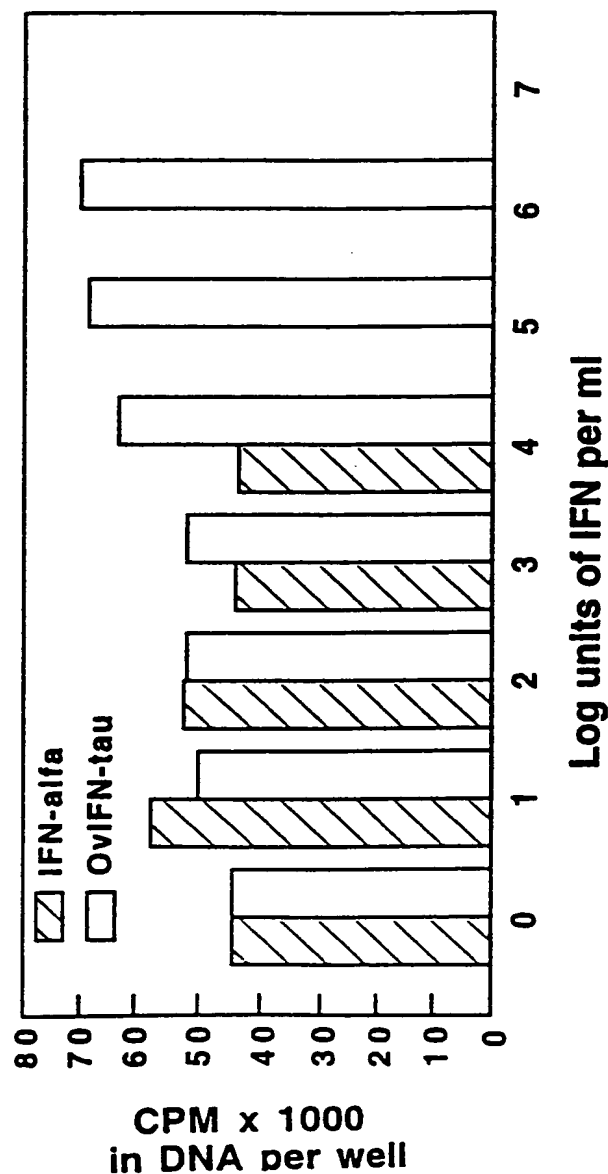
00221-01654260



Peptides	MW	HI*	Sequence
IFN $\alpha$ (1-37) (SEQ ID NO:5)	4465	-0.78	CYSLRKLMLDARENKLDRMNRRLSPHSCLQDRKDFG
IFN $\alpha$ (34-64) (SEQ ID NO:6)	3610	-0.72	KDFGLPQEMVEGDQLKDKQAFPLYEMLQQS
IFN $\alpha$ (62-92) (SEQ ID NO:7)	3586	-0.53	QQSFNLFYTEHSSAAWDTTLLLEQLCTGLQQQ
IFN $\alpha$ (90-122) (SEQ ID NO:8)	3712	-0.86	QQQLDHLDTCRGQVMGEEDSELGNMDPIVTVKK
IFN $\alpha$ (119-150) (SEQ ID NO:9)	3948	-0.56	TVKKYFQGIYDYLQEKGYSDCAWEIVRVEMMR
IFN $\alpha$ (139-172) (SEQ ID NO:10)	3818	-0.11	CAWEIVRVEMMRALTVSTTLQKRLTKMGGDLNSP

## Hydropathic Index

6. **பி.ரீ.**



**Fig. 8**

1  
CTGAGATGGGATCAGAGAACCTACCTGAAGGTTCCCCCTGACCCCATCTCAGCCAGCCCAGCAGCAGCCGCATCTTCCCC 80

81  
ATG GCC TTC GTG CTC TCT CTA CTG ATG GCC CTG GTG CTG GTC AGC TAT GGC CCA GGA GGA 140  
S1 Met Ala Phe Val Leu Ser Leu Leu Met Ala Leu Val Leu Val Ser Tyr Gly Pro Gly Gly S20  
141 TCT CTG GGT TGT TAC CTA TCT CGG AAA CTC ATG CTG GAT GCC AGG GAG AAC CTC AAG CTC 200  
S21 Ser Leu Gly Cys Tyr Leu Ser Arg Lys Leu Met Leu Asp Ala Arg Glu Asn Leu Lys Leu 17  
201 CTG GAC CGA ATG AAC AGA CTC TCC CCT CAT TCC TGT CTG CAG GAC AGA AAA GAC TTT GGT 260  
18 Leu Asp Arg Met Asn Arg Leu Ser Pro His Ser Cys Leu Gln Asp Arg Lys Asp Phe Gly 37  
261 CTT CCC CAG GAG ATG GTG GAG GGC GAC CAG CTC CAG AAG GAC CAG GCC TTC CCT GTG CTC 320  
38 Leu Pro Gln Glu Met Val Glu Gly Asp Gln Leu Gln Lys Asp Gln Ala Phe Pro Val Leu 57  
321 TAC GAG ATG CTC CAG CAG AGC TTC AAC CTC TTC TAC ACA GAG CAC TCC TCT GCT GCC TGG 380  
58 Tyr Glu Met Leu Gln Gln Ser Phe Asn Leu Phe Tyr Thr Glu His Ser Ser Ala Ala Trp 77  
381 GAC ACC ACC CTC CTG GAG CAG CTC TGC ACT GGA CTC CAA CAG CAG CTG GAC CAC CTG GAC 440  
78 Asp Thr Thr Leu Leu Glu Gln Leu Cys Thr Gly Leu Gln Gln Gln Leu Asp His Leu Asp 97  
441 ACC TGC AGG GGT CAA GTG ATG GGA GAG GAA GAC TCT GAA CTG GGT AAC ATG GAC CCC ATT 500  
98 Thr Cys Arg Gly Gln Val Met Gly Glu Glu Asp Ser Glu Leu Gly Asn Met Asp Pro Ile 117  
501 GTG ACC GTG AAG AAG TAC TTC CAG GGC ATC TAT GAC TAC CTG CAA GAG AAG GGA TAC AGC 560  
118 Val Thr Val Lys Lys Tyr Phe Gln Gly Ile Tyr Asp Try Leu Gln Gln Lys Gly Tyr Ser 137  
561 GAC TGC GCC TGG GAA ATC GTC AGA GTC GAG ATG ATG AGA GCC CTC ACT GTA TCA ACC ACC 620  
138 Asp Cys Ala Trp Glu Ile Val Arg Val Glu Met Met Arg Ala Leu Thr Val Ser Thr Thr 157  
621 TTG CAA AAA AGG TTA ACA AAG ATG GGT GGA GAT CTG AAC TCA CCT TGATGACTCTTGCCGACTA 666  
158 Leu Gln Lys Arg Leu Thr Lys Met Gly Gly Asp Leu Asn Ser Pro 172

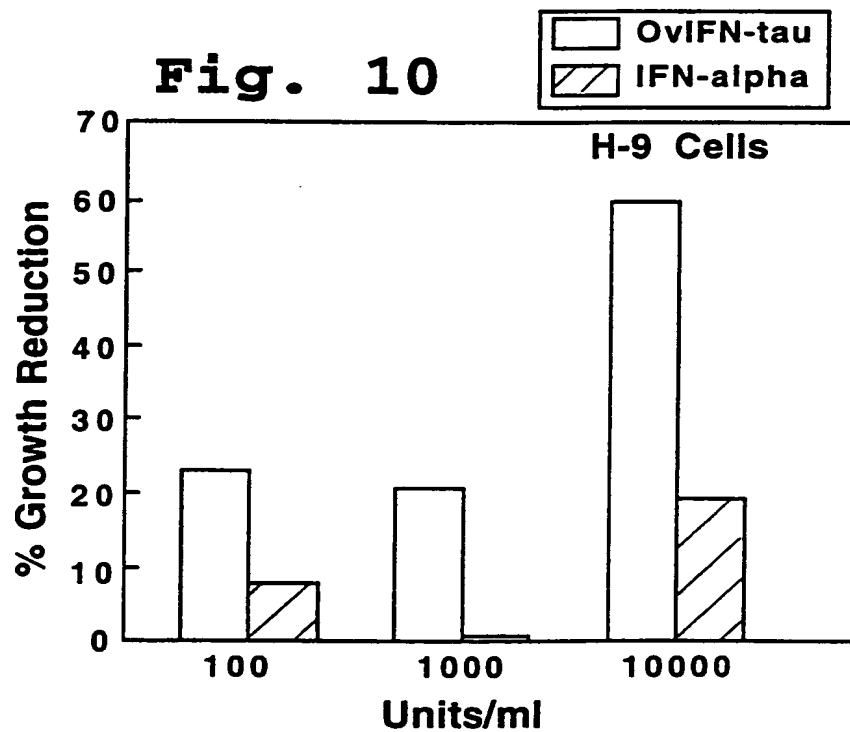
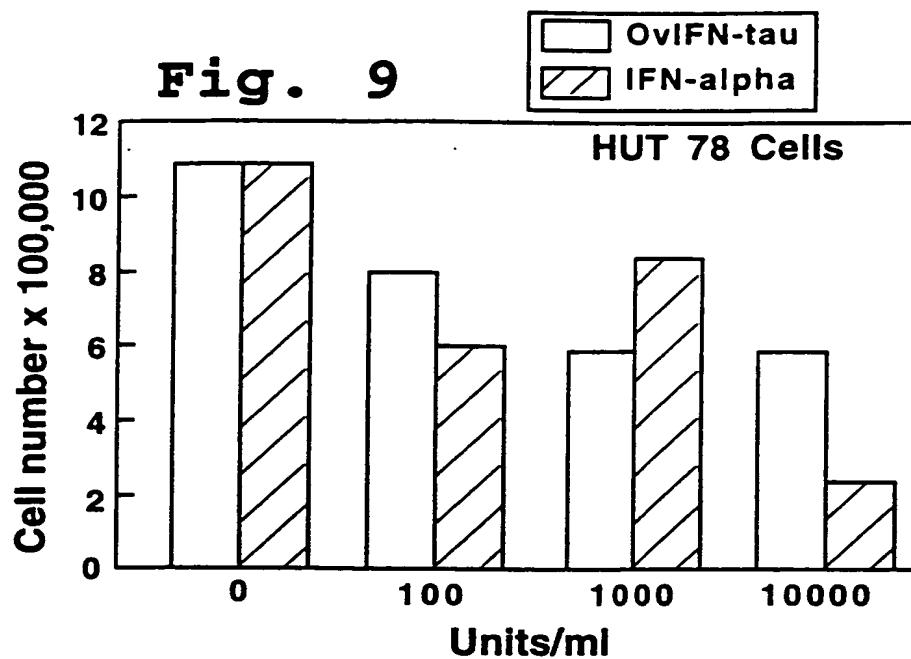
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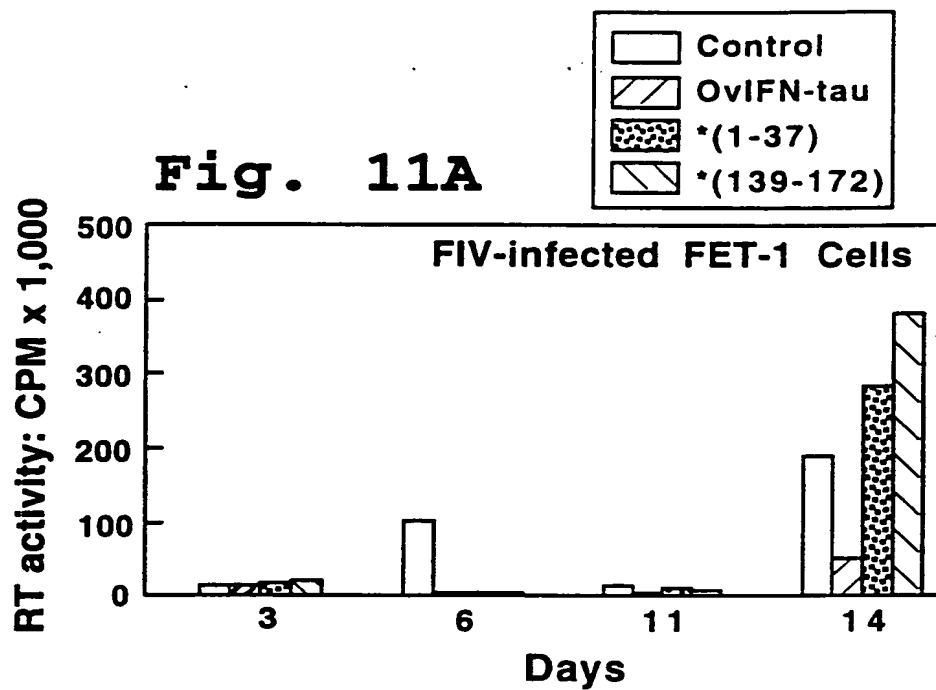
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TTGTTAAGTTACATTTACATCTGTACATCATATTAAAAATTTCTAAACAAAAA 972

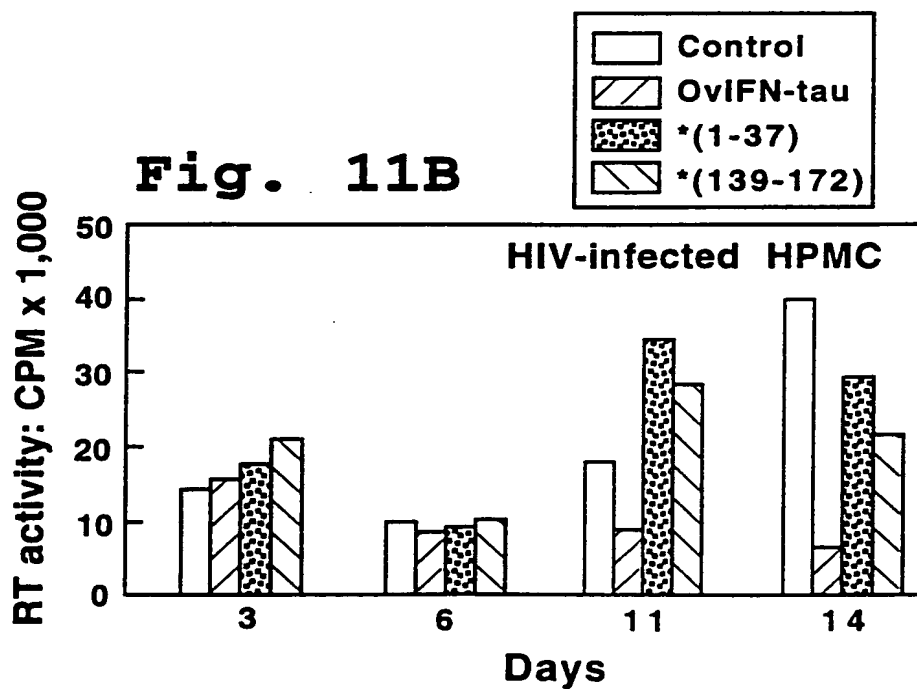
Fig. 7



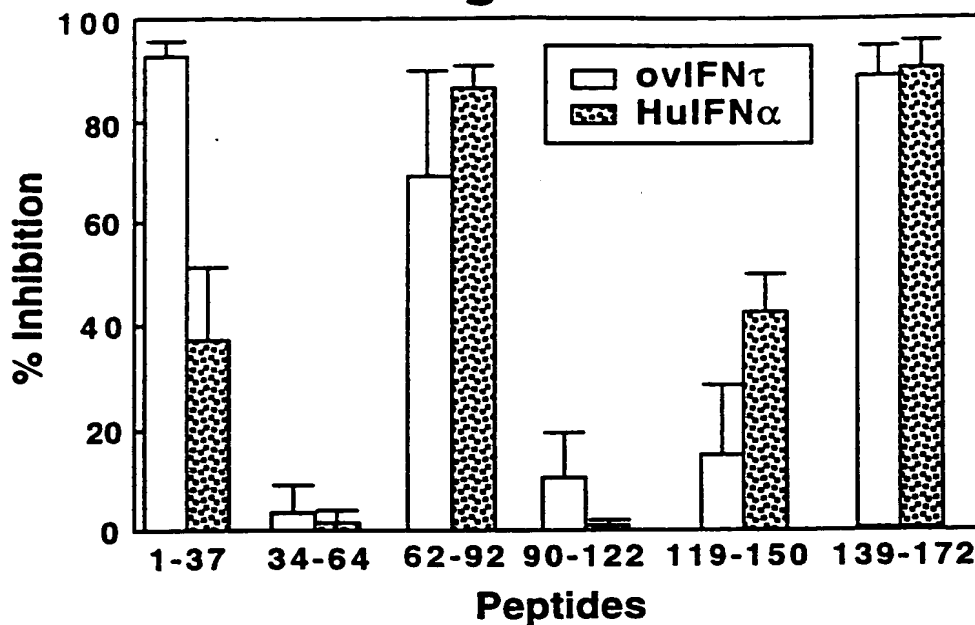
**Fig. 11A**



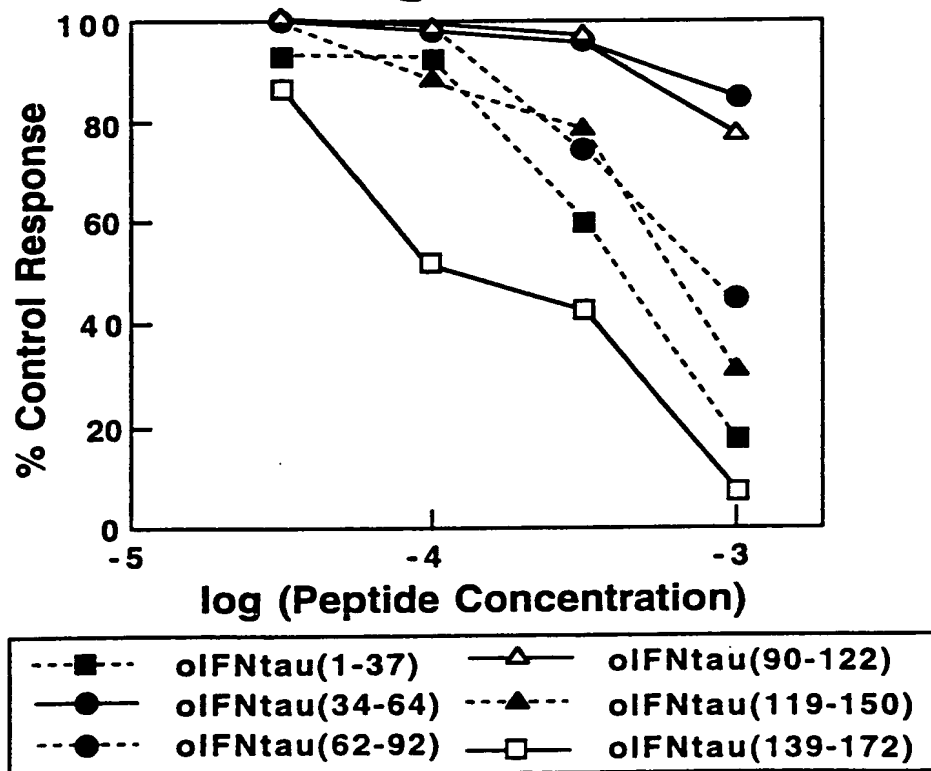
**Fig. 11B**



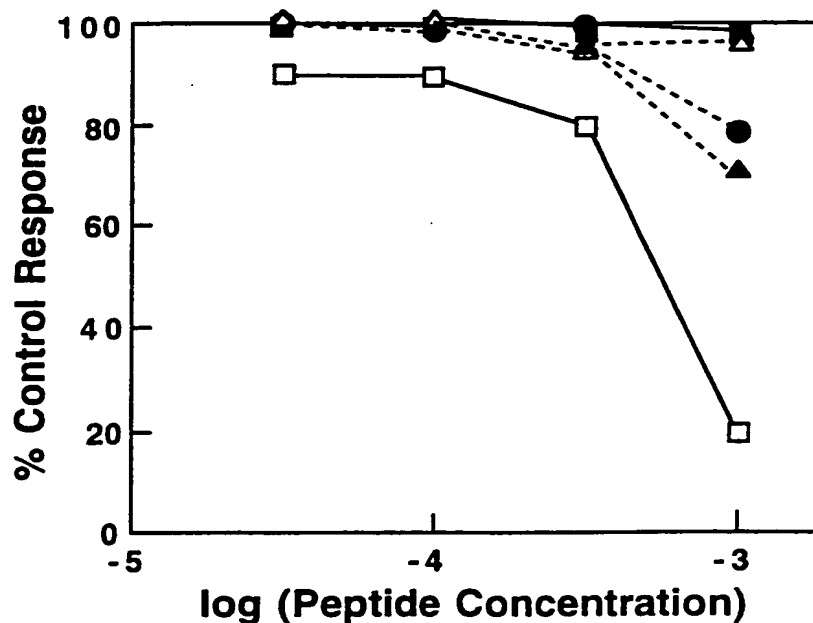
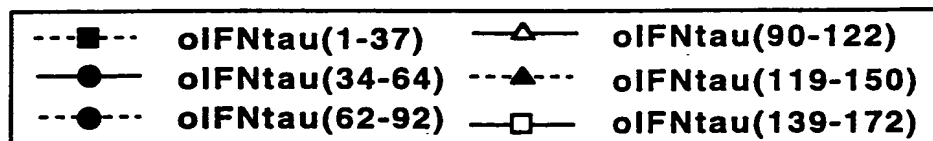
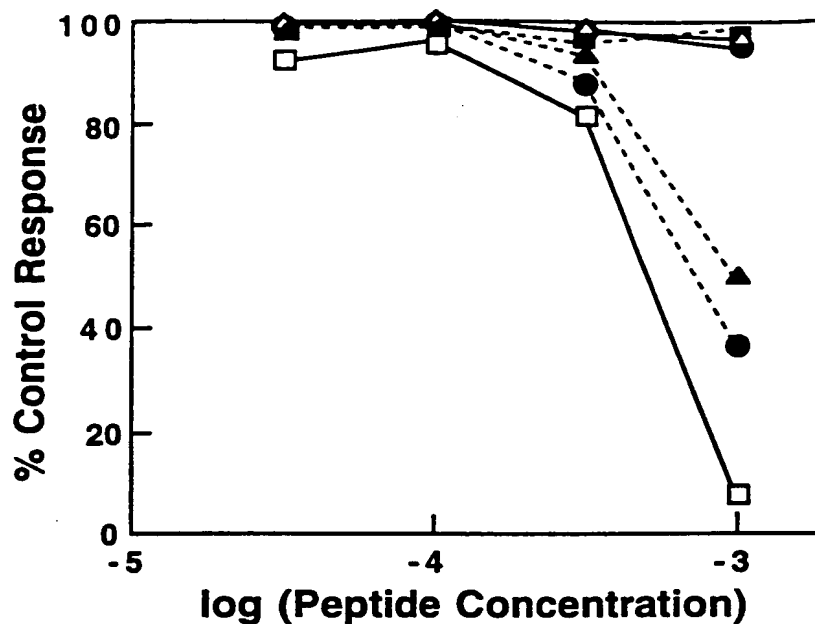
**Fig. 12**



**Fig. 13**

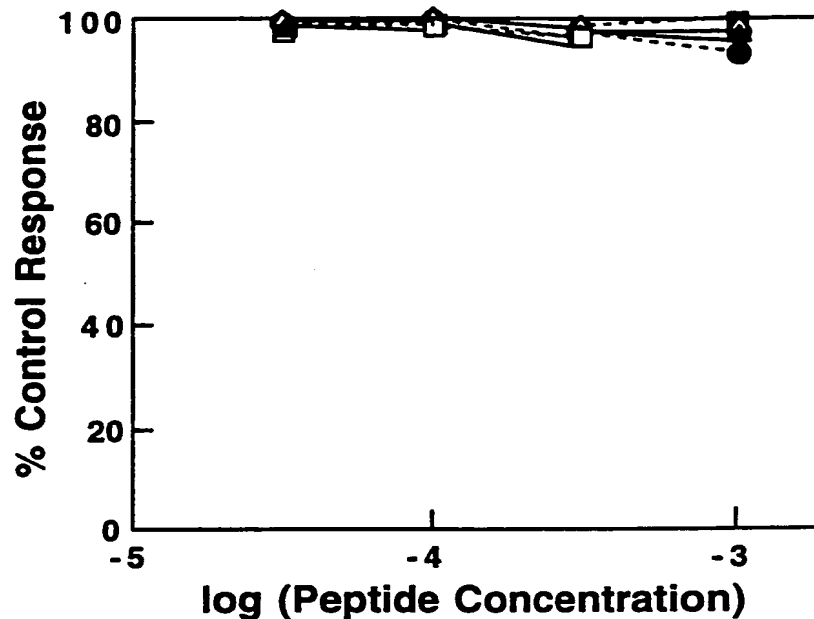
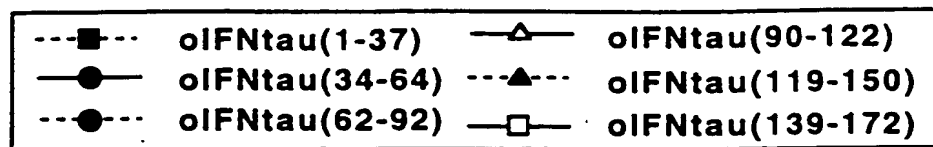


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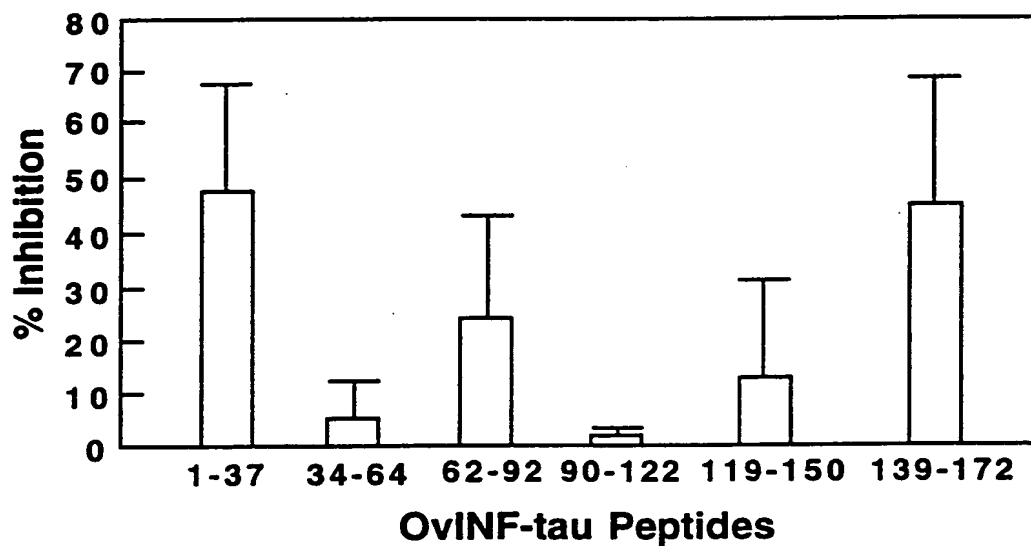


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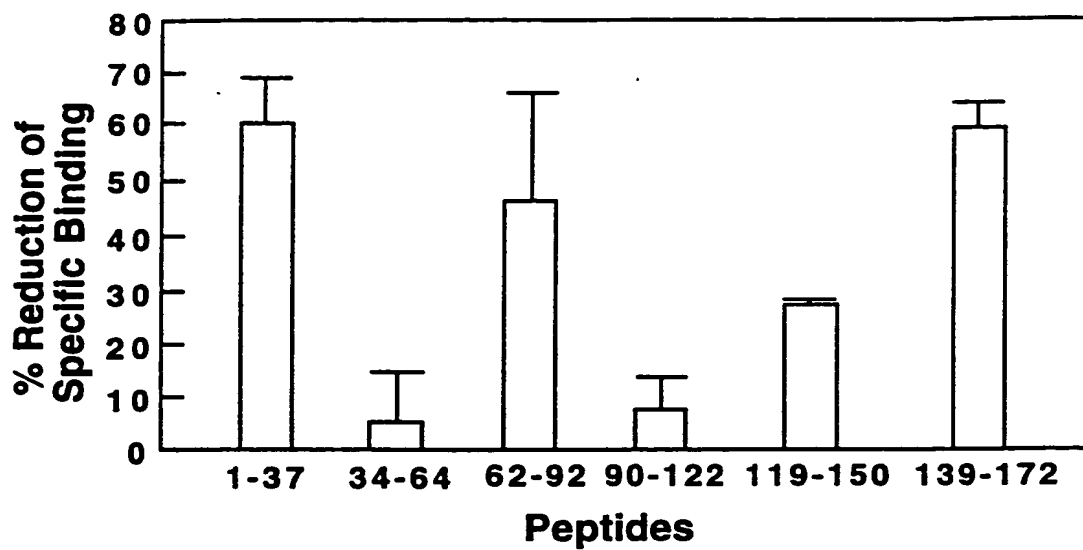
00221-07694250



**Fig. 16**



**Fig. 17**



**Fig. 18**

00222-67694/60



```

-23                                     -9
Met ala phe val leu ser leu leu met ala leu val leu val ser
oINft      cccc ATG GCC TTC GTG CTC TCT CTA CTG ATG GCC CTG GTG CTG GTC AGC
LEXY.5      cccc                                     c
TOSHI.9     cc                                     c
TOSHI.10    cc                                     c

-8                                     -1 +1                                     11
tyr gly pro gly gly ser leu gly cys tyr leu ser arg lys leu met leu asp ala
TAT GGC CCA GGA GGA TCT CTG GGT TGT TAC CTA TCT CGG AAA CTC ATG CTG GAT GCC
c                                     G g A C A G T G
c                                     (---)G g A C A G T G
c g c C G G g A C A G T G

12                                     20                                     30
arg glu asn leu lys leu leu asp arg met asn arg leu ser pro his ser cys leu
AGG GAG AAC CTC AAG CTC CTG GAC CGA ATG AAC AGA CTC TCC CCT CAT TCC TGT CTG
A G GA GG GC TT
A G A GG GC TT
C C G G A GG T GC T

31                                     40                                     49
gln asp arg lys asp phe gly leu pro gln glu met val glu gly asp gln leu gln
CAG GAC AGA AAA GAC TTT GGT CTT CCC CAG GAG ATG GTG GAG GGC GAC CAG CTC CAG
c C t a a a G
c C t a TAG a G
c C t a t G
Clone 21 ! t G
Clone 35 ! t G
Clone 15 ! G
Clone 18 ! T AG T

50                                     60                                     68
lys asp gln ala phe pro val leu tyr glu met leu gln gln ser phe asn leu phe
AAG GAC CAG GCC TTC CCT GTG CTC TAC GAG ATG CTC CAG CAG AGC TTC AAC CTC TTC
G C A T C T
G C A T C T
G C A T C
G C A T C
G C A T C A
G C A T T C T

69                                     80                                     87
tyr thr glu his ser ser ala ala try asp thr thr leu leu glu gln leu cys thr
TAC ACA GAG CAC TCC TCT GCT GCC TGG GAC ACC ACC CTC CTG GAG CAG CTC TGC ACT
C C C C C C C CT
C A G t

```

Fig. 19A

88 90 100 106  
gly leu gln gln gln leu asp his leu asp thr cys arg gly gln val met gly glu  
GGA CTC CAA CAG CAG CTG GAC CAC CTG GAC ACC TGC AGG GGT CAA GTG ATG GGA GAG  
T A t G CT g g  
T A t G CT g g  
T t G t G CT g g C  
T t G t G CT g g C  
T t G t G CT g g C  
T t G G CT g g C  
T t G t G t CT g g T CT

107 110 120 125  
glu asp ser glu leu gly asn met asp pro ile val thr val lys lys tyr phe gln  
GAA GAC TCT GAA CTG GGT AAC ATG GAC CCC ATT GTG ACC GTG AAG AAG TAC TTC CAG  
CC a GG C G CC C G T C G  
CC a GG C G CC C G T C G  
CC a GA C G CC C G A G t  
CC a GG C G CC C G A C t  
CC a GG C G CC C G A C t  
CC a GG C G CC C G GC  
CC a GG C G CC C G GC

126 130 140 144  
gly ile tyr asp tyr leu gln glu lys gly tyr ser asp cys ala trp glu ile val  
GGC ATC TAT GAC TAC CTG CAA GAG AAG GGA TAC AGC GAC TGC GCC TGG GAA ATC GTC  
C T A C  
C T A  
C T A t t  
C T A t t  
C T A !  
C AT !  
C T !

145 150 160 163  
arg val glu met met arg ala leu thr val ser thr thr leu gln lys arg leu thr  
AGA GTC GAG ATG ATG AGA GCC CTC ACT GTA TCA ACC ACC TTG CAA AAA AGG TTA ACA  
C G a C T T T TC T T G G G  
g a C T T T TC T T G G  
C G a C T t g T TC G C G

164 172  
lys met gly gly asp leu asn ser pro  
AAG ATG GGT GGA GAT CTG AAC TCA CCT TGA  
T A c G  
T A c G  
T A c G

Fig. 19B

```

-23                                     -9
oTP-1      Met ala phe val leu ser leu leu met ala leu val leu val ser
LEXY.5
TOSHI.9
TOSHI.10

-8                                -1 +1                                11
tyr gly pro gly gly ser leu gly cys tyr leu ser arg lys leu met leu asp ala
                                           asp          gln asn his val    val gly
                                           (---)asp       gln asn his val    val gly
                                           arg           asp       gln asn his val    val gly

12                                20                                30
arg glu asn leu lys leu leu asp arg met asn arg leu ser pro his ser cys leu
   lys              arg          glu        arg          arg phe
   lys              arg          gln        arg          arg phe
ser gln            arg          gly gln     arg          leu arg phe

31                                40                                49
gln asp arg lys asp phe gly leu pro gln glu met val glu gly asp gln leu gln
                           ala
                           ala      (Stop)             gly
                           ala             gly
Clone 21                    !                               gly
Clone 35                     !                             gly
Clone 15                     !                             gly
Clone 18                     !                         val ser    phe

50                                60                                68
lys asp gln ala phe pro val leu tyr glu met leu gln gln ser phe asn leu phe
glu ala         ile ser      his
glu ala         ile ser      his
glu ala         ile ser      his
glu ala         ile ser      his
glu ala         ile ser      his
glu ala         ile ser      his lys
glu ala         ile ser      his

69                                80                                87
tyr thr glu his ser ser ala ala try asp thr thr leu leu glu gln leu cys thr
his                                                    arg
his                                                    arg
his                                                    arg
his                                                    arg
his                                                    arg
his lys      arg                                       arg
his lys      arg                                       leu

```

**Fig. 20A**

**Fig. 20B**

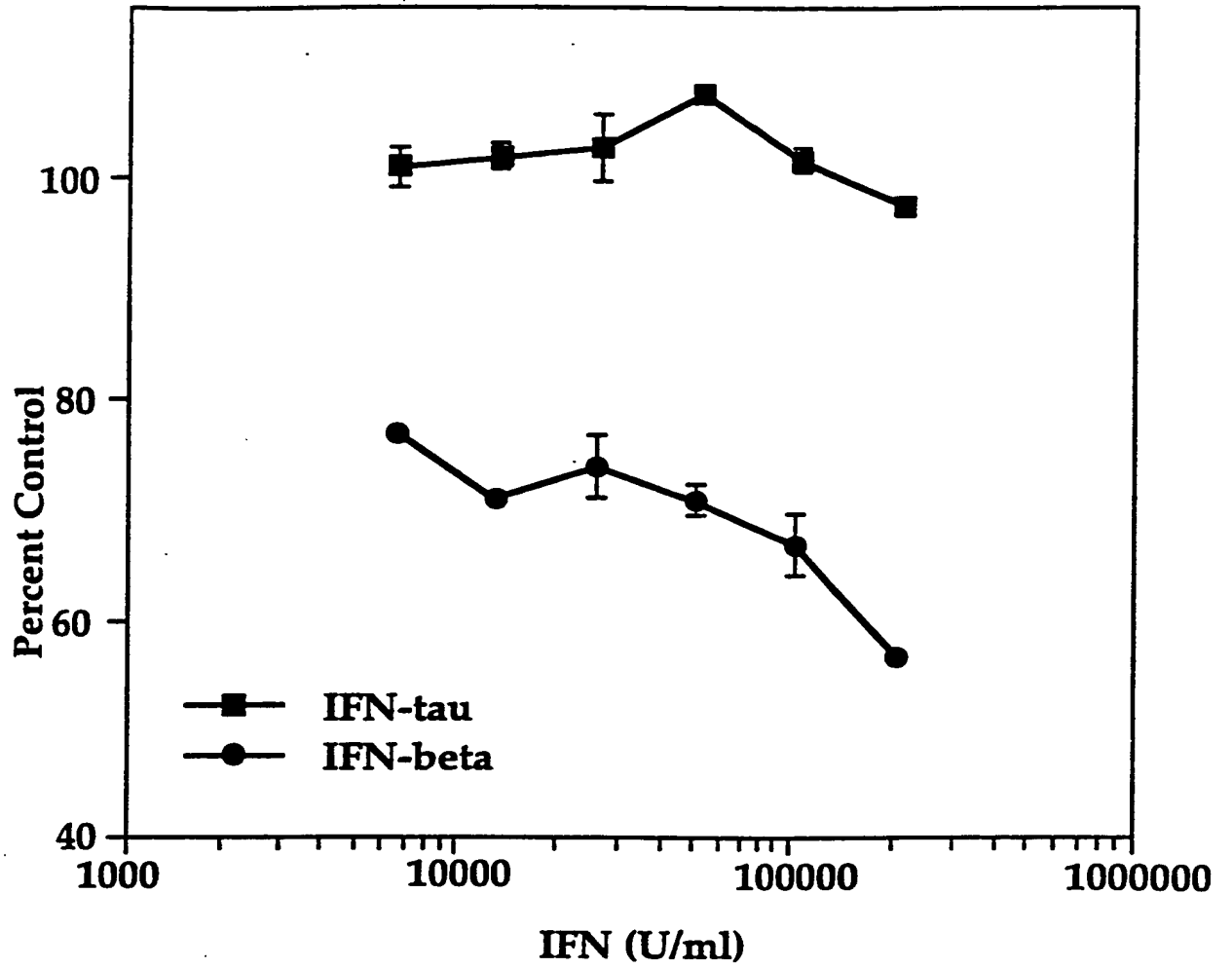


Fig. 21